possible activity that is detectable, each promoter sequence of said [,the] set of [different individual] promoter sequences comprising a double stranded DNA sequence [sequences], the sense strands of which comprise

at least two consensus sequences, said at least two consensus sequences corresponding to conserved sequences [of a promoter sequence] identified in said organism or group of organisms, at least half of each of said consensus sequences [is] being kept constant in the set of [all of the individual] promoter sequences and, between said consensus sequences or flanking at least one of said consensus sequences, [a] at least one nucleotide spacer sequence, at least part of which, relative to the corresponding spacer sequence of the identified promoter, is varied by substantially random incorporation of [to comprise] nucleotides that are selected [randomly among] from the group consisting of the nucleobases A, T, C and G,

the set of promoter sequences covering the range of [library spanning, with respect to] promoter activities for said gene [, a range of interest], in [small] steps, each step [preferably] changing the activity by 50-100%.

2. (Once Amended) A set of promoter sequences [promoter library] according to claim 1 wherein at least 10 nucleotides in the at least one nucleotide spacer sequence[(s)] are selected randomly [among] from the group consisting of the nucleobases A, T, C and G.

3. (Once Amended) A set of promoter sequences [promoter library] according to claim 1 wherein each of the promoter sequences comprise a regulatory DNA sequence imparting a specific regulatory feature to each of the [promoters of said] promoter sequences.

4. (Once Amended) A set of promoter sequences [promoter library] according to claim 1 wherein each of the promoter sequences comprises at least one recognition site for a restriction endonuclease.

5. (Once Amended) A set of promoter sequences [promoter library] according to claim 1 wherein the selected organism or group of organisms is selected from the group consisting of prokaryotic organisms.

6. (Once Amended) A set of promoter sequences [promoter library] according to claim 5 wherein the consensus sequences comprise at least 3 conserved nucleotides of the -10 signal TATAAT.

7. (Twice Amended) A set of promoter sequences [promoter library] according to claim 5 wherein the consensus sequences comprise at least 3 conserved nucleotides of the -35 signal TTGACA.

8. (Once Amended) A set of promoter sequences [promoter library] according to claim 5 wherein each of the promoter sequences comprise at least one conserved motif selected from the group consisting of AGTT at positions -44 to -41, TATTC at positions -40 to -35, TG at position -15 to -14 and GTACTGTT at positions +1 to +8 [consensus sequences further comprise intervening conserved motifs].

9. (Twice Amended) A set of promoter sequences [promoter library] according to claim 5 comprising at least two promoter sequences selected from the group consisting of [SEQ ID NO: 5 to SEQ ID NO: 42] SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34,

SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37,SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, and SEQ ID NO:42.

10. (Once Amended) A set of promoter sequences [promoter library] according to claim 7 wherein the spacer sequence between the -35 and the -10 signal is 14-23 bp.

11. (Once Amended) A set of promoter sequences [promoter library] according to claim 5 wherein the promoter sequences comprise a sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:2 [and minor variations hereof].

12. (Once Amended) A set of promoter sequences [promoter library] according to claim 1 wherein the selected organism or group of organisms is selected from the group consisting of eukaryotic organisms.

13. (Once Amended) A set of promoter sequences [promoter library] according to claim 12 wherein the consensus sequences comprise a TATA box and at least one upstream activation sequence (UAS).

SUB H1)

14. (Twice Amended) A set of promoter sequences [promoter library] according to claim 12 wherein the promoter sequence is [selected from the group consisting of] SEQ ID NO:3 [and minor variations hereof].

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15. (Twice Amended) A set of promoter sequences [promoter library] according to claim 12 comprising at least two promoter sequences selected from the group consisting of [SEQ ID NO: 43 to SEQ ID NO: 58] SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:58.

SUB H1)

16. (Once Amended) A method of constructing a set of [promoters (a promoter library)] promoter sequences which is suitable for optimizing the expression of a gene in a selected organism or group of organisms, the method comprising the steps of

(i) identifying in said organism or group of organisms a promoter sequence comprising at least two consensus sequences, which consensus sequences correspond to conserved sequences identified in said organism or group of organisms, at least one of the consensus sequences being flanked by a non-conserved nucleotide spacer sequence or both of said consensus sequences being separated by [a] the non-conserved nucleotide spacer sequence [(spacer sequence)],

(ii) constructing a set of single stranded DNA sequences comprising at least half of each of the consensus sequences [of the identified promoter sequence], and a non-conserved nucleotide spacer sequence, at least part of which[, relative to the spacer sequence of the identified promoter,] is varied by a substantially random incorporation of [to comprise] nucleotides [that are selected randomly among] selected from the group consisting of the nucleobases A, T, C and G, whilst keeping the at least half of the consensus sequences constant, and

(iii) converting the single stranded DNA sequences into double stranded DNA sequences to obtain [a] the set of [different promoters] promoter sequences covering, with respect to promoter strength, a range of promoter activities which is within a range from the weakest possible activity that is detectable to the strongest possibly activity that is detectable.

17. (Twice Amended) A method according to claim 16 wherein the set of promoter sequences [different promoters] obtained [is a promoter library] spans [spanning], with respect to promoter activities for said gene, the [a] range [of interest] in [small] steps, each step [preferably] changing the activity by 50-100%.

18. (Twice Amended) A method of optimizing the expression of a gene in an organism, the method comprising

(i) selecting from the set of promoter sequences [promoter library] of [any of] claim 1 a [set of promoters] plurality of promoter sequences covering a desired range of promoter activities,

(ii) [cloning] transforming said set of promoter[s] sequences into cells of the organism, placing in each [clone] of said cells the gene to be expressed under the control of at least one promoter of the set,

(iii) cultivating the [clones] transformed cells to obtain clones thereof and selecting among said clones a clone showing an optimal level of gene expression [optimized flux of gene product formation].

19. (Once Amended) A method according to claim 18 wherein the increase in activity from one promoter sequence to [an] at least one other promoter sequence of the set of promoter[s] sequences is [in steps that do not exceed] 50-100%.

21. (Twice Amended) A method of isolating a promoter sequence being capable of optimizing the expression of a gene in a selected organism, the method comprising

(i) constructing, using the method of claim 16, a set of promoters covering, with respect to promoter strength, a range of promoter activities which is within a range from the weakest possible activity that is detectable to the strongest possible activity is detectable,

(ii) [cloning] transforming said set of promoters into cells of the selected organism, placing in each of said cells [clone] the gene to be expressed under the control of at least one promoter of the set,

(iii) cultivating the transformed cells to obtain clones thereof and selecting among said clones a [the] clone showing optimal level of gene expression [optimized flux of gene product formation], and

(iv) isolating said promoter sequence from the clone showing optimal level of gene expression [optimized flux of gene product formation].

22. (Once Amended) A promoter sequence [that is capable of optimizing the expression of a gene in a selected organism, the promoter sequence is obtainable by the method of claims 21] selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57 and SEQ ID NO:58.